

SCORE Search Results Details for Application 10663794 and Search Result us-10-663-794-2.rup.

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This page gives you Search Results detail for the Application 10663794 and Search Result us-10-663-794-2.rup.

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OM protein - protein search, using sw model

Run on: May 1, 2006, 18:30:37 ; Search time 231 Seconds
(without alignments)
784.938 Million cell updates/sec

Title: US-10-663-794-2
Perfect score: 1313
Sequence: 1 MLKFKYGARNPLDAGAAEPI.....VDFGSAAKMNSNKMVKNGIR 257

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1287	98.0	2027	1 CTRO_HUMAN	O14578 homo sapien
2	1183	90.1	448	2 O88527_RAT	O88527 rattus norv
3	1180	89.9	2055	1 CTRO_MOUSE	P49025 mus musculu
4	845.5	64.4	472	2 Q4T429_TETNG	Q4t429 tetraodon n
5	557.5	42.5	1854	2 Q9VTY8_DROME	Q9vty8 drosophila
6	531	40.4	717	2 Q8AVM0_XENLA	Q8avm0 xenopus lae
7	531	40.4	1551	2 Q6DT37_HUMAN	Q6dt37 homo sapien

8	529	40.3	1354	1	ROCK1_HUMAN	Q13464	homo sapien
9	529	40.3	1354	1	ROCK1_MOUSE	P70335	mus musculu
10	529	40.3	1354	1	ROCK1_RABIT	O77819	o rho-assoc
11	529	40.3	1369	1	ROCK1_RAT	Q63644	rattus norv
12	526	40.1	1166	2	Q61XJ4_CAEBR	Q61xj4	caenorhabdi
13	524	39.9	1401	2	Q5SP91_BRARE	Q5sp91	brachydanio
14	520.5	39.6	174	2	Q4T424_TETNG	Q4t424	tetraodon n
15	520	39.6	492	2	Q86XZ8_HUMAN	Q86xz8	homo sapien
16	520	39.6	933	2	Q86TJ1_HUMAN	Q86tj1	homo sapien
17	520	39.6	1173	2	P92199_CAEL	P92199	caenorhabdi
18	520	39.6	1711	2	Q9Y5S2_HUMAN	Q9y5s2	homo sapien
19	520	39.6	1760	2	Q9ULU5_HUMAN	Q9ulu5	homo sapien
20	519	39.5	1370	2	O73732_XENLA	O73732	xenopus lae
21	519	39.5	1708	2	Q5TZ42_BRARE	Q5tz42	brachydanio
22	511.5	39.0	1388	1	ROCK2_HUMAN	O75116	homo sapien
23	511	38.9	1702	2	O54875_RAT	O54875	rattus norv
24	511	38.9	1713	2	Q7TT49_RAT	Q7tt49	rattus norv
25	510	38.8	605	2	Q6DI71_MOUSE	Q6di71	mus musculu
26	510	38.8	631	1	DMPK_MOUSE	P54265	mus musculu
27	508	38.7	1713	2	Q7TT50_MOUSE	Q7tt50	mus musculu
28	507	38.6	1388	1	ROCK2_BOVIN	Q28021	bos taurus
29	506	38.5	1739	2	Q4T2A9_TETNG	Q4t2a9	tetraodon n
30	504	38.4	629	2	Q6P5Z6_HUMAN	Q6p5z6	homo sapien
31	502	38.2	1379	1	ROCK2_RAT	Q62868	rattus norv
32	502	38.2	1388	1	ROCK2_MOUSE	P70336	mus musculu
33	500	38.1	1533	2	Q4S6S5_TETNG	Q4s6s5	tetraodon n
34	499	38.0	1375	2	Q4SLR2_TETNG	Q4slr2	tetraodon n
35	495	37.7	1375	2	Q90Y37_BRARE	Q90y37	brachydanio
36	494.5	37.7	1592	2	O01583_CAEL	O01583	caenorhabdi
37	493.5	37.6	1716	2	Q5TZ37_BRARE	Q5tz37	brachydanio
38	487.5	37.1	1586	2	Q60X12_CAEBR	Q60x12	caenorhabdi
39	487	37.1	1337	2	Q53SJ7_HUMAN	Q53sj7	homo sapien
40	485.5	37.0	1702	2	Q59GZ1_HUMAN	Q59gz1	homo sapien
41	484	36.9	1382	2	Q4SK04_TETNG	Q4sk04	tetraodon n
42	484	36.9	1732	2	O54874_RAT	O54874	rattus norv
43	482	36.7	496	2	Q99646_HUMAN	Q99646	homo sapien
44	482	36.7	1638	2	Q86XX2_HUMAN	Q86xx2	homo sapien
45	482	36.7	1638	2	Q8IWQ7_HUMAN	Q8iwq7	homo sapien

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OM protein - protein search, using sw model

Run on: May 1, 2006, 18:33:47 ; Search time 40 Seconds
(without alignments)
618.193 Million cell updates/sec

Title: US-10-663-794-2
Perfect score: 1313
Sequence: 1 MLKFKYGARNPLDAGAAEPI.....VDFGSAAKMNSNKMVKNGIR 257

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	529	40.3	1354	2	S74244	serine/threonine-s
2	529	40.3	1354	2	S69211	serine/threonine-s
3	520	39.6	1173	2	T25539	hypothetical prote
4	511	38.9	1702	2	T14050	protein kinase (EC
5	510	38.8	557	2	S71829	serine/threonine-s
6	507	38.6	1388	2	S70633	serine/threonine-s
7	504	38.4	624	2	B49364	protein kinase (EC
8	502	38.2	1388	2	S74245	serine/threonine-s
9	494.5	37.7	1548	2	T25808	hypothetical prote
10	484	36.9	1732	2	T14039	protein kinase (EC
11	433	33.0	522	2	G86431	protein kinase T5I
12	412	31.4	465	2	I38133	protein kinase (EC

13	410.5	31.3	756	2	S60966	probable protein k
14	408.5	31.1	596	2	F84589	probable protein k
15	407.5	31.0	469	2	T41723	serine/threonine-s
16	406.5	31.0	479	2	S42864	protein kinase (EC
17	404	30.8	483	2	T05188	protein kinase F4I
18	399.5	30.4	569	2	A86170	hypothetical prote
19	393.5	30.0	545	2	T01288	protein kinase F27
20	393	29.9	526	2	S49077	protein kinase PKT
21	392	29.9	480	2	T47255	serine/threonine k
22	392	29.9	598	2	T47254	serine/threonine k
23	392	29.9	620	2	S22711	probable protein k
24	391.5	29.8	443	2	D71405	probable protein k
25	391.5	29.8	475	2	H85156	protein kinase [im
26	389.5	29.7	1356	2	T16718	hypothetical prote
27	389	29.6	500	2	S42867	protein kinase (EC
28	382.5	29.1	665	2	S70706	probable protein k
29	377	28.7	1099	2	A56155	tumor suppressor p
30	375.5	28.6	908	2	T25035	hypothetical prote
31	364.5	27.8	564	2	S59776	protein kinase DBF
32	353.5	26.9	572	2	S64387	protein kinase DBF
33	353	26.9	624	2	T41341	probable serine-th
34	348	26.5	412	2	I78395	myotonic dystrophy
35	348	26.5	441	2	I78393	myotonic dystrophy
36	348	26.5	474	2	I78396	myotonic dystrophy
37	348	26.5	516	2	I78394	myotonic dystrophy
38	337	25.7	480	2	S56639	ribosomal protein
39	337	25.7	607	2	S62556	probable serine/th
40	334.5	25.5	465	2	S68462	protein kinase ATP
41	333.5	25.4	425	2	S41099	protein kinase (EC
42	329	25.1	1770	2	S56221	hypothetical prote
43	327.5	24.9	471	2	S68463	protein kinase ATP
44	327	24.9	1338	2	T40993	protein kinase cek
45	321	24.4	436	2	JC4516	protein kinase (EC

SCORE Search Results Details for Application 10663794 and Search Result us-10-663-794-2.rapbn.

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OM protein - protein search, using sw model

Run on: May 1, 2006, 18:39:17 ; Search time 26 Seconds
(without alignments)
449.531 Million cell updates/sec

Title: US-10-663-794-2
Perfect score: 1313
Sequence: 1 MLKFKYGARNPLDAGAAEPI.....VDFGSAAKMNSNKMVKNGIR 257

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 232119 seqs, 45477862 residues

Total number of hits satisfying chosen parameters: 232119

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /SIDS5/ptodata/1/pubpaa/US08_NEW_PUB.pep1:*
2: /SIDS5/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /SIDS5/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /SIDS5/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /SIDS5/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /SIDS5/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
7: /SIDS5/ptodata/1/pubpaa/US09_NEW_PUB.pep1:*
8: /SIDS5/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
9: /SIDS5/ptodata/1/pubpaa/US10_NEW_PUB.pep1:*
10: /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
11: /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB.pep1:*
12: /SIDS5/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
1	1313	100.0	257	9	US-10-663-794-2	Sequence 2, Appli
2	1270	96.7	2053	9	US-10-877-346-11	Sequence 11, Appl
3	1270	96.7	2066	9	US-10-877-346-9	Sequence 9, Appli
4	1183	90.1	251	9	US-10-663-794-4	Sequence 4, Appli
5	1180	89.9	251	9	US-10-663-794-5	Sequence 5, Appli
6	1180	89.9	251	9	US-10-663-794-6	Sequence 6, Appli
7	531	40.4	1197	9	US-10-055-877-8	Sequence 8, Appli
8	531	40.4	1247	9	US-10-055-877-10	Sequence 10, Appl
9	511.5	39.0	1388	9	US-10-501-035-350	Sequence 350, App
10	511	38.9	1663	9	US-10-055-877-148	Sequence 148, App
11	494.5	37.7	1590	9	US-10-055-877-146	Sequence 146, App
12	484	36.9	1732	9	US-10-055-877-147	Sequence 147, App
13	480	36.6	1613	9	US-10-055-877-145	Sequence 145, App
14	480	36.6	1637	9	US-10-055-877-144	Sequence 144, App
15	470.5	35.8	639	11	US-11-113-837-21	Sequence 21, Appl
16	433	33.0	522	11	US-11-188-298-15746	Sequence 15746, A
17	433	33.0	562	11	US-11-188-298-11972	Sequence 11972, A
18	419	31.9	566	11	US-11-188-298-6803	Sequence 6803, Ap
19	418	31.8	555	11	US-11-188-298-3933	Sequence 3933, Ap
20	415.5	31.6	548	11	US-11-188-298-12757	Sequence 12757, A
21	413	31.5	461	11	US-11-188-298-4091	Sequence 4091, Ap
22	412	31.4	556	11	US-11-188-298-13437	Sequence 13437, A
23	411	31.3	556	11	US-11-188-298-1509	Sequence 1509, Ap
24	410.5	31.3	522	11	US-11-188-298-8728	Sequence 8728, Ap
25	410.5	31.3	756	11	US-11-113-837-20	Sequence 20, Appl
26	410	31.2	629	11	US-11-188-298-6634	Sequence 6634, Ap
27	408.5	31.1	438	11	US-11-188-298-1619	Sequence 1619, Ap
28	408.5	31.1	596	11	US-11-188-298-17865	Sequence 17865, A
29	408	31.1	416	11	US-11-188-298-9559	Sequence 9559, Ap
30	408	31.1	465	11	US-11-096-568A-5519	Sequence 5519, Ap
31	408	31.1	483	11	US-11-096-568A-5518	Sequence 5518, Ap
32	408	31.1	495	11	US-11-188-298-20770	Sequence 20770, A
33	408	31.1	503	11	US-11-096-568A-5517	Sequence 5517, Ap
34	408	31.1	512	11	US-11-188-298-4973	Sequence 4973, Ap
35	408	31.1	515	11	US-11-188-298-7362	Sequence 7362, Ap
36	408	31.1	515	11	US-11-188-298-20448	Sequence 20448, A
37	408	31.1	518	11	US-11-188-298-21632	Sequence 21632, A
38	408	31.1	541	11	US-11-188-298-1885	Sequence 1885, Ap
39	407.5	31.0	501	11	US-11-188-298-20542	Sequence 20542, A
40	407.5	31.0	525	11	US-11-188-298-11915	Sequence 11915, A
41	407.5	31.0	555	11	US-11-188-298-21317	Sequence 21317, A
42	407.5	31.0	585	11	US-11-188-298-2999	Sequence 2999, Ap
43	406.5	31.0	479	11	US-11-188-298-20695	Sequence 20695, A
44	406.5	31.0	564	11	US-11-188-298-17432	Sequence 17432, A
45	404.5	30.8	545	11	US-11-188-298-5522	Sequence 5522, Ap

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OM protein - protein search, using sw model

Run on: May 1, 2006, 18:37:42 ; Search time 47 Seconds
(without alignments)
452.078 Million cell updates/sec

Title: US-10-663-794-2
Perfect score: 1313
Sequence: 1 MLKFKYGARNPLDAGAAEPI.....VDFGSAAKMNSNKMVKNGIR 257

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1313	100.0	257	2	US-09-916-204-2
2	1313	100.0	257	2	US-10-282-048-2
3	1287	98.0	1958	2	US-10-028-946-4

4	1287	98.0	2054	2	US-10-028-946-2	Sequence 2, Appli
5	1284	97.8	497	2	US-09-804-471A-2	Sequence 2, Appli
6	1284	97.8	497	2	US-10-238-709-2	Sequence 2, Appli
7	1284	97.8	497	2	US-10-724-594-2	Sequence 2, Appli
8	1277	97.3	2053	2	US-10-017-216-2	Sequence 2, Appli
9	1270	96.7	2053	2	US-09-964-956-11	Sequence 11, Appl
10	1270	96.7	2066	2	US-09-964-956-9	Sequence 9, Appli
11	1183	90.1	251	2	US-09-916-204-4	Sequence 4, Appli
12	1183	90.1	251	2	US-10-282-048-4	Sequence 4, Appli
13	1180	89.9	251	2	US-09-916-204-5	Sequence 5, Appli
14	1180	89.9	251	2	US-09-916-204-6	Sequence 6, Appli
15	1180	89.9	251	2	US-10-282-048-5	Sequence 5, Appli
16	1180	89.9	251	2	US-10-282-048-6	Sequence 6, Appli
17	1180	89.9	494	2	US-09-804-471A-4	Sequence 4, Appli
18	1180	89.9	494	2	US-10-238-709-4	Sequence 4, Appli
19	1180	89.9	494	2	US-10-724-594-4	Sequence 4, Appli
20	1180	89.9	2055	2	US-10-017-216-4	Sequence 4, Appli
21	529	40.3	420	2	US-08-685-871-58	Sequence 58, Appl
22	529	40.3	1354	2	US-08-685-871-2	Sequence 2, Appli
23	520	39.6	330	2	US-09-771-161A-128	Sequence 128, App
24	520	39.6	1711	2	US-09-771-161A-219	Sequence 219, App
25	520	39.6	1711	2	US-09-771-161A-220	Sequence 220, App
26	515	39.2	246	2	US-09-771-161A-129	Sequence 129, App
27	511.5	39.0	1388	1	US-08-685-576-4	Sequence 4, Appli
28	511.5	39.0	1388	2	US-09-976-594-296	Sequence 296, App
29	507	38.6	1388	1	US-08-685-576-1	Sequence 1, Appli
30	504	38.4	625	2	US-09-771-161A-242	Sequence 242, App
31	504	38.4	625	2	US-09-771-161A-243	Sequence 243, App
32	497	37.9	420	2	US-08-685-871-59	Sequence 59, Appl
33	485.5	37.0	509	2	US-09-949-016-8511	Sequence 8511, Ap
34	482	36.7	496	2	US-09-771-161A-228	Sequence 228, App
35	470.5	35.8	639	2	US-10-100-252-21	Sequence 21, Appl
36	469	35.7	582	1	US-08-422-699A-9	Sequence 9, Appli
37	469	35.7	582	1	US-08-422-706B-9	Sequence 9, Appli
38	448.5	34.2	638	1	US-08-422-699A-11	Sequence 11, Appl
39	448.5	34.2	638	1	US-08-422-706B-11	Sequence 11, Appl
40	435	33.1	900	1	US-08-630-822A-62	Sequence 62, Appl
41	435	33.1	900	1	US-09-005-069-62	Sequence 62, Appl
42	435	33.1	900	2	US-09-171-156A-21	Sequence 21, Appl
43	435	33.1	900	2	US-09-004-730A-21	Sequence 21, Appl
44	435	33.1	900	2	US-08-981-799A-21	Sequence 21, Appl
45	412	31.4	336	2	US-09-771-161A-180	Sequence 180, App

SCORE Search Results Details for Application 10663794 and Search Result us-10-663-794-2.rag.

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OM protein - protein search, using sw model

Run on: May 1, 2006, 18:29:57 ; Search time 187 Seconds
(without alignments)
603.852 Million cell updates/sec

Title: US-10-663-794-2
Perfect score: 1313
Sequence: 1 MLKFKYGARNPLDAGAAEPI.....VDFGSAAKMNSNKMVKNGIR 257

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID	Description	

1	1313	100.0	257	7	ADJ79947	Adj79947	Human kin
2	1287	98.0	319	7	ADN62730	Adn62730	Human cit
3	1287	98.0	495	6	ABP97681	Abp97681	Amino aci
4	1287	98.0	497	5	AAE16261	Aae16261	Human kin
5	1287	98.0	497	6	ABP97687	Abp97687	Amino aci
6	1287	98.0	620	8	ADN62809	Adn62809	Human NOV
7	1287	98.0	623	6	ADA05644	Ada05644	Human NOV
8	1287	98.0	1958	5	ABB81928	Abb81928	Human kin
9	1287	98.0	2054	5	ABB81927	Abb81927	Human kin
10	1287	98.0	2054	5	AAE24150	Aae24150	Human kin
11	1287	98.0	2054	6	AAO26959	Aao26959	Human CRI
12	1284	97.8	497	6	ABU10127	Abu10127	Variant n
13	1284	97.8	497	6	ABU10126	Abu10126	Novel hum
14	1284	97.8	497	7	AAE39504	Aae39504	Human kin
15	1284	97.8	497	8	ADO40592	Ado40592	Human kin
16	1277	97.3	2053	5	AAE24079	Aae24079	Human MDP
17	1277	97.3	2053	7	ADF60994	Adf60994	Pain asso
18	1277	97.3	2053	8	ADQ89100	Adq89100	Human uro
19	1270	96.7	2053	5	ABG78363	Abg78363	RHO/RAC-i
20	1270	96.7	2053	6	ADA05642	Ada05642	Human NOV
21	1270	96.7	2053	8	ADN63228	Adn63228	Human NOV
22	1270	96.7	2053	8	ADN62807	Adn62807	Human NOV
23	1270	96.7	2066	5	ABG78362	Abg78362	Human pro
24	1270	96.7	2066	6	ADA05654	Ada05654	Human NOV
25	1270	96.7	2066	8	ADN62819	Adn62819	Human NOV
26	1265.5	96.4	2053	4	AAU03501	Aau03501	Human pro
27	1265.5	96.4	2055	8	ADJ96610	Adj96610	Human cit
28	1262	96.1	349	4	ABG15566	Abg15566	Novel hum
29	1183	90.1	251	7	ADJ79949	Adj79949	Rat kinas
30	1180	89.9	251	7	ADJ79950	Adj79950	Mouse kin
31	1180	89.9	494	6	ABP97682	Abp97682	Polypepti
32	1180	89.9	494	8	ADO40594	Ado40594	Mouse cit
33	1180	89.9	2055	6	ABP97683	Abp97683	Polypepti
34	1180	89.9	2055	6	AAO26960	Aao26960	Human CRI
35	660	50.3	144	7	ADJ79951	Adj79951	Mouse kin
36	557.5	42.5	1252	4	ABB66357	Abb66357	Drosophil
37	535	40.7	821	6	ABP96051	Abp96051	Human pro
38	531	40.4	475	5	AAE24131	Aae24131	Human kin
39	531	40.4	1197	6	ABJ37881	Abj37881	NOVX prot
40	531	40.4	1247	6	ABJ37882	Abj37882	NOVX prot
41	531	40.4	1551	8	ADI40850	Adi40850	Human kin
42	531	40.4	1553	7	ADC99064	Adc99064	Human KPP
43	531	40.4	1565	8	ADP47967	Adp47967	Human MRC
44	531	40.4	1569	8	ADF95102	Adf95102	Human ser
45	531	40.4	1572	5	AAE19162	Aae19162	Human kin